Tue Jan 17 09:42:59 2006

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Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USFTO spool/US10751235/runat 12012006 120916 2538/app query.fasta_1.263
-Q=/cgn2_1/USFTO spool/US10751235/runat 12012006 110916 2538/app query.fasta_1.263
-DEJESUGG_PATENTE = NA -QFMT=fastap -SUFFIX=p2n.mi -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=51ts -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLENE=0 -MAXLENE=200000000
-USER=US10751235 @CGN_1 1 193 @runat_12012006 120916 2538 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELCOK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 7, Appli
Sequence 5, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 11, Appli
                                                                                                                                    January 15, 2006, 12:59:30; Search time 171 Seconds (without alignments) 800.423 Million cell updates/sec
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                                                                                                                                                                                                                                                                                   1 LOPYAEDGSAVNMEAKFSOM.....SIDLLPYWKIDALCKIVPRQ 77
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Sequence 1
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1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq:*

7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*

8: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                          - nucleic search, using frame_plus_p2n model
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US-09-615-192A-156
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CURRENT APPLICATION NUMBER: US/09/615,192A

CURRENT FILING DATE: 2000-07-12

PRIOR PILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: US 08/75,316

PRIOR PILING DATE: 1996-09-11

PRIOR PILING DATE: 1996-09

NUMBER OF SEQ ID NOS: 405

SOOFWARE: PastSEQ for Windows Version 3.0

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LENGTH: 404
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Sequence 156, Application US/09615192A
Patent No. 6410718
GENERAL INFORMATION:
APPLICANT: Blokeberg, Leonard N.
APPLICANT: Havukkala, Ilkka
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58.21$
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50.89%
    TELEFAX: 919-854-1401
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1831 base pairs
                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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                     31 GTTGACATGGAGGCAGAATTTTCAAATCTAGCTTTGGACATTATTGGATTGTGTGTATTT
                                                                            31 AsnIyrAsnPheAspSerLeuThrThrAspSerProValIleGluAlaValTyrThrAla
11 ValAsnMetGluAlaLysPheSerGlnMetThrLeuAspVallleGlyLeuSerLeuPhe
                                                                                                                                                                                                                                                                                                                                                Sequence 156, Application US/09169789
; Sequence 156, Application US/09169789
; Patent No. 6653528
; GENERAL INFORMATION:
    APPLICANT: Bloksberg, Leonard N.
    APPLICANT: Bloksberg, Likka
    TITLE OF INVENTION: Materials and Methods for the
    TITLE OF INVENTION: Modification of Plant Lignin Content;
    FILE REFERRENCE: 11000.1003-2
; CURRENT FILING DATE: 1999-10-09
    EARLIER APPLICATION NUMBER: US 08/975,316
    EARLIER PILING DATE: 1997-11-21
    SARLIER PILING DATE: 1996-09-11
    NUMBER: OF SEQ ID NOS: 185
    SOFTWARE: FREING PATE: 1996-09-11
    NUMBER: PREING DATE: 1996-09-11
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    LENGTH: 404
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211 AGATGGTTAGTTCCTCGCCAA 231
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is Sequence 3, Application US/10018730A
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igeneral information:
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ORGANISM: Pinus radiata
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Best Local Similarity:
Query Match:
DB:
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seed protein yield.

US2004216190-A1 Viridiplantae.

28-OCT-2004.

18-DEC-2003; 2003US-00739930 28-APR-2003; 2003US-00424599. 28-APR-2003; 2003US-00425115.

(KOVA/) KOVALIC D K.

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                                     1681 TCTCTAATTATTCATGAACTAAATTTTCTGATTGATTTGTTTCCTGGTAGGTCTTGATAA
                                                                        1741 GAAGAGCTCAAGTTCCTGACATTCTTCCTGGGAACTATAAGGTCAATACCGGACAAGACA
                                                                                                                                                      1801 TTATGATTTCAGTCTATAACATCCATGTTCTTCCGAGGTACAGTTCTCTTCTTCTCTC
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ADT15447 standard; cDNA; 3377

ADT15447;

(first entry) 13-JAN-2005

Plant cDNA, Seg ID 773.

Plant; ss; gene; transgenic; cold tolerance; growth rate; drought tolerance; disease resistance; galactomannan production; plant growth regulator; heat tolerance; herbicide tolerance; lignin production; extreme osmoctic condition tolerance; pathogens resistance; pest resistance; yield improvement; seed oil yield; RESULT 4
APT15447
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AC APT17
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The invention relates a recombinant DNA construct comprising a CDA The invention relates a recombinant DNA construct comprising a Dolypeptide with any of 5544 amino acid sequences (Dolywoll-cotide harving any of 5544 muclectide sequences (SEQ ID NO: 5454-11088). The CDNAs and proteins are from corn, soybean, Arabidopsis, wheat and rape but the specification does not indicate which sequences is derived from which organism. Also included is a method of producing a plant harling an improved property, comprising transforming a plant with a recombinant DNA construct comprising transforming a plant with a recombinant DNA construct comprising transforming a plant with a recombinant DNA construct comprising transforming a plant with a recombinant DNA construct comprising transforming a plant with a selected from improving plant coll tolerance. For manipulating growth requised from improving plant collerance to plant disease, for galactomannan production, for production cof plant proving plant tolerance to herbicides, for increasing the rate of manipulating growth requised from improving plant tolerance to pathogens or pests, for yield improvement by modification of plant tolerance to extreme osmetic conditions, for improving plant tolerance to extreme osmetic conditions, for improving plant tolerance to pathogens or pests, for yield improvement by modification of carbohydrate, introgen or phosphorus use and/or uptake and for yield improvement by modification of carbohydrate, introgen or phosphorus use and/or uptake and for yield improvement by providing improved plant growth and development under at least one stress condition. The polymulation and for yield improvement by providing improved plant growth and development under at least one stress condition. The polymulation and for yield improvement by providing improved plant growth improved collegeneties, in particular for producing transgenic plants with improved biological characteristics such as increased yield, improved biological characteristics such as increased New recombinant DNA constructs useful in the field of biochemistry and genetics, and in particular for producing transgenic plants with improved biological characteristics. Claim 1; SEQ ID NO 773; 14pp; English. WPI; 2004-757369/74.

Sequence 3377 BP; 967 A; 729 C; 736 G; 945 T; 0 U; 0 Other;

Indels 494; 32.5%; Score 803; DB 13; Length 3377; ilarity 73.2%; Pred. No. 1.1e-208; Conservative 0; Mismatches 0; Indels 494. Best Local Similarity Matches 1347; Conserv Query Match

79 AIGGAGICTICACICTITICTCCCATCTICCTCTTACTCTTCTTCTTCACTGCAAA 138 1 ATGGAGTCTTCACTCTTTTCTCCATCTTCCTCTTTACTCTTCTCTCTTCACTGCAAAA

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SUMMARIES	a a	ATT4D2	AY424805	AY091083	AF367289	ATH526463	AK220829	BT012891	AP008216 208	AC025783	AE017117	AK065689	AC155564	AY142017	AY058173	AY056446	AK068163	AC155503	CR954209_3
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ALIGNMENTS

•	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. Nyakatura,G., Fartmann,B., Dauner,D., Sterr,W., Holland,R., Weichselgartner,M., Mewes,H.W., Lemcke,K., Mayer,K.F.X., Quetier,F.	and Stationat, m. Unpublished (bases 1 to 92611) (conditional to 92611)	<pre>d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2 rue Gaston Cremieux, BP191, 91006 Bvry Cedex, Prance; http://www.genoscope.cns.fr Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4</pre>	and a can	/ecctype="Columbia" 20812646 /gene="T4D2.10" join(20812434,25332646) /gene="T4D2.10"
RESULT 1 14714D2 1COUS DEFINITION ACCESSION YERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	JOURNAL REFERENCE AUTHORS TITLE JOURNAL	COMMENT	FEATURES BOUTCE	gene

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1131. 6090,6168. 6490,6606. 6884,6997. 7249,7359. 7529,
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QHQKIQAREIHCMQTCFKIILESINSNDQGYNFCSLAVGTSEDSKTWACQTRRWVSLC
SFLLTECNYSQERIKDVIGWALLLRILIVLTDPKSWKIITWENFEDAETAKKIIQP
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AVBEYVSLILTIPRLVCYLPSALIRALKHKSILMPSFHTILLLKOKILNIISEMENSB
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SPGPREHVBCTTSDQPGSGQVNESTNDVMDVFTLRGGPVGISKEVSCLLHLFCATYAHL
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YERDCRHPFCASALMLSPSRTSRPPLAPARTHBVLPFDDVLTTPSMGSVTI TPHVP
PFERVHYFREF I SKOMSRÄMGGENDAPGARS I EI VYRKGHYWEDGFQQLNSI GSRL
KSSI HVSFVNRSGGLBERGLDYGGLSKRFLTDI TKAAPATKTRGLFSQTPFSDRLLVVPS
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YRALMYCHYDGDLKELCLDFTVTEBFCGKMSI I ELKDGGRYDFWTMSKRMYY I TAKMAYVKHYDGDLKELCDFTVTEBFCGKMSI I ELKDGGRYDFWTMSKRMYY TGGYSDSSRTIXI PREWMKGFBFSRCLLLKFVTSCSRAFLLGFKYLQFTFIIHKVSC DTSLWAAIGGDVBRLPSASTCYNTLKLPTYKRASTWRRKLLYAITSNAGFELS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="similarity to KIAA0010 protein, Homo sapiens
// note="similarity to BETA-GALACTOSIDASE PRECURSOR,
Lycopersicon esculentum, gb:P48980"
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gene="T4D2.10"
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gene="T4D2.20"
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/note="strong similarity
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Matches 2467; Conservative 0;
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BGPLWTARRARAVVPSHRYLLSVYTBRYPCKCABELVBEYLOPYCAPSOSSAVNBEAKFSO
WALDVIGLSLFNYNFDSLTTDSPVIEAVYTALKEABELRSTDLLPYWIJDALCKTVPRO
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                                                                                                                                                                       /codon_start=1
/product="chloroplast carotenoid epsilon-ring hydroxylase"
                                                                                                                                                                                                                                                                                                                                   VQLRDDLLSMLVAGHETTGSVLTWTLYLLSKNSSALRKAQEEVDRVLEGRNPAFEDIK
ELKYITRCINESMRLYPHPPVLIRRAQVPDILPGNYKNTGQDIMISYYNIHRSSEVW
EKAEEFLPERFDIDGAIPNETWTDFKFIPFSGGPRKCVGDQFALMEAIVALAVFLQRL
NVELVPDQTISMTTGATIHTTNGLYMKVSQR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
32.5%; Score 803; DB 15;
Best Local Similarity 73.2%; Pred. No. 4.7e-182;
Matches 1347; Conservative 0; Mismatches 0;
                                                                                                                                                                                                  /protein_id="AARB3120.1"
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                       organism="Arabidopsis
                                     /mol_type="mRNA"
/db_xref="taxon:3702"
                                                                      /chromosome="3"
/ecotype="Columbia"
1. .1620
                                                                                                                                                        gene="LUT1"
                                                                                                                     /gene="LUT1"
[. .1620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (Brass I to 1620)
Tian, L., Musetti, V., Kim, J., Magallanes-Lundback, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Arabidopsis LUT1 locus encodes a member of the cytochrome P450 family that is required for carotenoid epsilon-ring hydroxylation
                                                      GTTGTTTGTTATTCCAAAGGTATGGGAAAAAGCTGAGGAATTTCTGCTGAACGATTCGA
                                                                                                                    CATAGATGGCGCAATCCCCTAACGAAACAAACACTGATTTCAAGTAAACTCAGTAGAACAC
                                                                                                                                                                                            18920 CATAGATGGCGCAATCCCTAACGAAACAAACACTGATTTCAAGTAAACTCAGTAGAACAC
                                                                                                                                                                                                                               2101 ATCTTTTGACACAAACTACTGAATCAAGATTAGTGGTTTTGATTAGGGAATTTAAAAGAT
                                                                                                                                                                                                                                                 ATATCTAACCGGAGTGGACAITCCTAGTAITACAITCAIGCCCACAITICITAIGIGITI
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Submitted (30-SEP-2003) Biochemistry and Molecular Biology,
Michigan State University, East Lansing, MI 48824, USA
Location/Qualifiers
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Tian.L., Musetti,V., Kim,J., Magallanes-Lundback,M.
DellaPenna,D.
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